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>*CtManS* -1964 bp.

GGAATTCGGCACGAGGTGCC TGCAACAAGTCAC TAGTCCATCCTGCAGTTCCCTAACCCT
CCCTAGTGTCTTTCTCTTCAGGCTCCATATTCCTTTATAACTACTACAATAGATACAATG
AGAAACCTAATCTTCGAGGAGCCTGAAGGGATTCCAGGCAACAGTTCAAGCAGTCTGCGC
TATGCC TGGCAATCAATTCGTGCCCCAGTGATCATACTCTTCTAAAAC TAGCAGTCATA
GTGTGCTCAGTTATGTCAATCATGCTATTTGTTGAAAGAGTAGCCATGGCAGCTGTAATT
TTGATTGTCAAAGTGCTGAGGAAGAAAAGATACACCAAGTATAACTTGGGAAGCCATGAAA
CAGAAGCTAGAGAGAAGCAAAAATACCCCATGGTGCTGATCCAAATACCTATGTATAAC
GAGAAAGAGGTGTACAAGCTTTCCATTGGAGCAGTATGTGGGCTTTTCATGGCCAGCTGAC
AGGTTTCATAGTTCAAGTTCTTGATGACTCAACAAATCCAGTCTTAAGGGAGTTGGTTGAA
ATGGAGTGTCAAAAATGGATACAGAAAGGTGTGAATGTCAAGTATGAAAATAGGAGAAAT
CGCAATGGTTACAAAGCAGGTGCCTTAAAAGAGGGTTTGGAGAAGCAATATGTAGAGGAT
TGTGAGTTTGTAGCAATATTTGATGCAGATTTCCAACCAGATGCGGATTTTCTTTGGAAC
ACAATTCCTTATCTGCTGGAAAATCCAAAGTTGGGTTTGGTTCAGGCGAGATGGAAATTT
GTGAAC TCAGAAGAATGTATGATGACACGGCTTCAAGAGATGTCAC TAGATTACCACTTT
AGTGTGTAACAGGAAGTCGGCTCTTCAACATACTCATTTCTTCGGTTTCAATGGAACAGCA
GGAGTTTGGCGGATCCAAGCCATAAAAGATGCTGGAGGATGGAAAGACCGAACAACGGTG
GAGGATATGGACCTTGCAGTTAGAGCAAGCTTGCATGGCTGGGAATTTGTTTTTGTGGGT
GATGTAAAGGTCAAAAATGAATTACCAAGTACATTTAAAGCATATCGATTT CAGCAGCAC
AGGTGGTCATGCGGTCCAGCTAATCTCTTTAAGAAAATGACCAAGGAAATCATCTGTTGC
AAAAGGGTGCCACTTCTCAAGAGACTCCATCTCATCTATGCTTTCTTCTTTGTGAGAAA
ATAGTTGCACACTGGGTTACGTTCTTCTTTTACTGCATAGTTATACCAGCTTGTGTGATA
GTTCCCGAAGTTAATCTCAAAAAGCAGATTGCCATATACATCCCAGCAACCATTACAATT
CTAAATGCAGTCTCCACCCCAAGATCCATGCATCTACTAGTACTCTGGATACTCTTTGAG
AATGTCATGTCACTCCATCGAACTAAAGCAGCAATTATTGGACTCTTGGGAAGCAAATCGT
GTCAATGAATGGGTGTGACTGAGAAGCTTGGAAATGCCATGAAACAGAGGAACAATGCT
AGGCCATCAAGAGCTTACGGTTTTCGAATTATAGAAAGGATCCACCCATTGGAGATTATA
GTGGGGATGTATATGCTGCACTGTGCAACCTATGACCTGTTATTTCGGACACGACCATTTCT
TTTGTCTATCTTCTGTTGCAGGCAGGGGCGTTCTTTACAATGGGATTTGGCCTAGTAGGA
ACAATTGTACCCACCTAAAGCTTAAAGGTCATGGACTCATGAACATAAGTATTAGTGTAT
GAACGGGTCTGTTTGTTTTAAAGACTCTAAGTCTAGTGAAC TAGCTATCCATAAGCATAG
AACTGTAAGAGAAGCTACGGCTACTTAGTAGAAGCATTCCATATGGTATCAGGACTTCTT
TGTACCCATGTATAAGAACCAGAATCAAAACGTATAAACATGTCCATAATATGAAGCTTA
AATAAATCTGTTATCTGCAC TAAAAAAAAAAAAAAAAAAAAAAC

FIGURE 1

>CiMANS - 526 aa.

MRNLIFEEPEGIPGNSSSSSLRYAWQSIRAPVIIPLLKLAVIVCSVMSIMLFVERVAMAAV
ILIVKVLRRKKRYTKYNLEAMKQKLEERSKKYPMVLIQIPMYNEKEVYKLSIGAVCGLSWPA
DRFIVQVLDDSTNPVLRRELVEMECQKWIQKGVNVKYENRRNRNGYKAGALKEGLEKQYVE
DCEFVAIFDADFQPDADFLWNTIPYLLENPKLGLVQARWKFNSEECMMTRLQEMSLDYH
FSVEQEVGSSTYSFFGFNGTAGVWRIQAIKDAGGWKDRTTVEDMDLAVRASLHGWEFVFV
GDVKVKNELPSTFKAYRFQQHRWSCGPANLFKKMTKEIICCKRVPLLKRLHLIYAFFFVR
KIVAHWVTFFFYCIVIPACVIVPEVNLKKQIAIYIPATITILNAVSTPRSMHLLVLWILF
ENVMSLHRTKAAIIGLLEANRVNEWVTEKLGNAMQQRNNARPSRASRFRIIERIHPLEI
IVGMYMLHCATYDLLFGHDHFFVYLLLQAGAFFTMGFGLVGTIVPT

FIGURE 2

>*CtGalT2* - 1609 bp.

GGAATTTCGGCACGAGGC'TCCCATGGCGAAATCCTCCAATTCCAGAAACAAAATTTACACAC
GTAAACCTCTCCGACGGTTTCCCTCTTCCCTCGCCGGAGCATTCTCCGCGCTTCTAATCGTT
TGGGGTTTCTCCTCCTTCACAACCCCCATCCCTAACGAAACCCCAACCTTCGAATCACTT
TCGGTAAATTCTCACCAAAACGACGCCGT'TTCGCGCGGGGGACCGGATT'TCCGGTTTCGAT
CCCCCGGACCGGACTT'TCTACGACGACCCGAAATGGGGTACACCATAGACACGACGGTG
CGAGATTGGGATGCAAAGCGTGAGGAGTGGCTGCGGCTTCATCCTTCCCTTCGCCGCCGGA
GCGAGAGAACGAGTTTTGGTGGTGACCGGATCGCAGCCGGCACCGTGCCGGAATCCCATC
GGCGACCAC'TTGC'TGTTACGGTTTTTTAAGAACAAGGTGGATTACTGTTCGGTTACACGGG
TACGATATCGTGTAACAATGCATTGTTACACCCGAAAATGTTTACGTATTGGGCGAAG
TACCCGGTGGTGCGGGCCGCGATGATGGCCCCACCCGGAAGCCGAGTGGATCTGGTGGGTC
GACTCGGACGCGTTGTTTACCGACATGGAGTTCAAAC'TACCATTAGATCACTACAAGGAT
CACAACCTCGTCGTCCATGGCTGGGCCCACCTCATCCACGAGAAACG'TAGTTGGACGGGC
CTCAACGCCGGCGTCTTCC'TCATCAGAAACTGTCAATGGTCATTGGACTTCATAAACGAA
TGGGCCAGCATGGGCCCACAAACTCCGAACTACGAGAAATGGGGTCAAACCC'TAAAGTCA
ACTTTCAAAGACAAATTTCTTCCCGGAGTCAGACGATCAGACGGGCCTCGCTTACCTGATC
GCGATCGAGAAAGAAAAATGGGCGGACAAGATTTACTTAGAGAACTCGTATTATTTTCGAA
GGGTACTGGGAAGAAATCGTCGGAACATTCGAGAATATAAGCAAGAAATACAACGAGATC
GAAACGGGGGTGCGCAGGTTAAGAAGGCGTCACGCGGAGAAAGTGAGTGAAGCTTACGGT
GAAGAGAGGGAGAAATATTTAACGGAAGCAGGTAACGGTAAAGGAAGCTGGAGACGGCCG
TTTGTGACGCAC'TTACGGGGTGTCAACCTTGTAGCGGAAAATATAACGCTATGTATAAC
GCCGAAGATTGTTGGAACGGAATGCGTAAAGCCCTTAATTTTCGCTGATAATCAGGTGATG
CGTAAATATGGTTTTCGTACACCCGGATGTACTAGATAATTCCGTTTTCGCCGATTCCGTTT
GATTATCCCCGTAACCGCTCAGGTAATAATCATATTTAATGGAATCTAATTATTGTTGAC
CGCTGGCTACTCAGATTCTCCATGTGTTCTGTAAAGTACTAGTACTACTAGTATTAAATT
TCTTAGTGTATATTTTATAATATTTTATTGTATATTTTCTGGCGTTTTGCATATATAGT
ATCGTGTGGAGTAGTATTTAATTATGCATAAGTGAAGGGATAATTTTATTCTTTTCGAAT
CCCTAACT

FIGURE 3

>CtGALT2 - 445 aa.

MAKSSNSRNKISHVNLSDGFLFLAGAFSAFLIVWGFSSFTTPIPNETPTFESLSVNSHQN
DAVSRGGPDFRFDPPDRTFYDDPEMGYTIDTTVRDWDAKREEWRLHPSFAAGARERVLV
VTGSQPAPCRNPIGDHLLLRFFKNKVDYCRLHGYDIVYNNALLHPKMFTYWAKYPVVRAA
MMAHPEAEWIIWVDSALFTDMEVXLPLDHYKDHNLVVHGWAHLIHEKRSWTGLNAGVFL
IRNCQWSLDFINEWASMGPTPNYEKGQTLKSTFKDKFFPESDDQTGLAYLIAIEKEKW
ADKIYLENSYYFEGYWEEIVGTFENISKYNEIETGVRRLRRRHAEKVSEAYGEEREKYL
TEAGNGKGSWRRPFVTHFTGCQPCSGKYNAMYNAEDCWNGMRKALNFADNQVMRKYGFVH
PDVLDNSVSPIPFDYPRNRSGNNHI

FIGURE 4

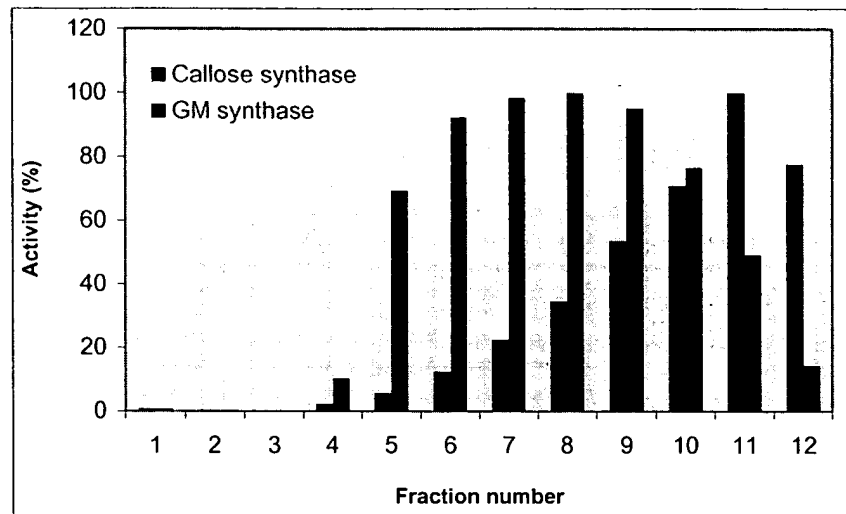


FIGURE 5

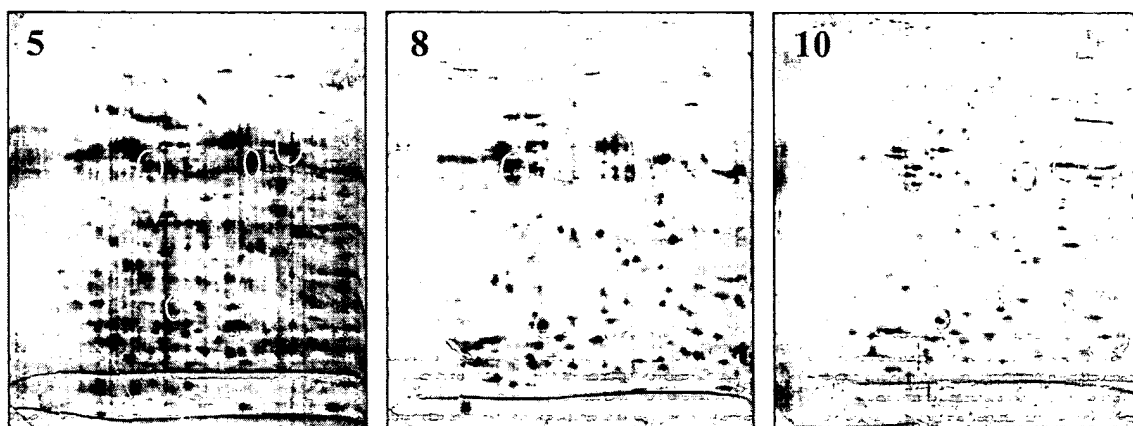


FIGURE 6

		1	60
Fenugreek	(1)	-----GCGACGAAATTGG-----	
Guar-GalT1	(1)	GGAAATTCGGCAGGAGCTCCAGTATCAATCACTCACTCCCATGGCCAAATTGG-----	
Guar-GalT2	(1)	-----GGAATTGGCAGGAGCTCCCATGGCGAAATCTCCAAT	
Consensus	(1)	G A C CTCCCATGGCGAAATTGG T	
		61	120
Fenugreek	(16)	TCCRAAAACAAATCCTCTCC--ATGGCTCTCAAATGGTTGCATCTTCTCTCTAGGTGCA	
Guar-GalT1	(58)	TCCAGAAACAAATCCTCTAA--ATGGATCTCCAACGGTTGGTGCTTCTCTCTAGGAGCA	
Guar-GalT2	(40)	TCCAGAAACAAATTTACACGTAACCTCTCCGACGGTTTCTCTTCTCTGCGCGAGCA	
Consensus	(61)	TCCAGAAACAAATCCTCTCA ATGGCTCTCCAACGGTTGC TCTTCTCTCTAGGAGCA	
		121	180
Fenugreek	(73)	ATGTCAGCTCTTCTTATGATTTGGGGGCTCAATTCCTTCATCGTCCAAATCCCAAACTCC	
Guar-GalT1	(115)	TTCACTGCTCTTCTTCTGCTCTGGGGTTTATGCTCCTTCATCATCCCCATCCCAAAACCC	
Guar-GalT2	(100)	TTCTCCGCGCTTCTAATCGTTTGGGGTTTCTCTCCTTCAACACCCCATCCCTAACGAA	
Consensus	(121)	TTCTC GCTCTTCTTATG TTGGGGTTTCT CTCCTTCATCACCCCATCCCAAAAC CC	
		181	240
Fenugreek	(133)	AACCCAAATTCAACTCCGTTGACCACCAAACTCAAATCCTTAAACTTCACCACAAACACG	
Guar-GalT1	(175)	GACCCCAAGCTCAACTCCGTCGCCACCACTTTGAGATCCCTTAACCTTCCCAAAACCCG	
Guar-GalT2	(160)	ACCCCAACCTTCGAATGAC-----TCGGTAATCTCAACCAAAACGAC	
Consensus	(181)	AACCCAAA TTCAACTCC TC CCACCA T T A ATCC TAAACTTTCCCAAAAC CC	
		241	300
Fenugreek	(193)	A----AC-TTTGCTGGTCTGATTTGTACATGACCCCTTCAGACAAACCTTCTATGAT	
Guar-GalT1	(235)	GCTGCCAC-CITGCC--TCCCACTTGGAGCAGCACCCCTCCTGACACACCTTCTACGAC	
Guar-GalT2	(205)	GCGTTTTCGGCGGGGACCGGATTTCCGGTTGGATCCCGGACCGGACTTCTACGAC	
Consensus	(241)	GC G AC CTTC GGTCC GATTTGC GCACGACCTCC GACA ACCTTCTACGAC	
		301	360
Fenugreek	(247)	GATCCAGAAATGTTTACACCATGATGGACAAACCAATGAAAAATTGGGATGAGAAGCGT	
Guar-GalT1	(292)	GACCCCGAAACAGTTTATACCAT---GGACAAACCAATGAAAAACTGGGACGAGAAGCGT	
Guar-GalT2	(265)	GACCCGAAATGGGGTACACCAT---AGACACGACGGTCCGAGATTGGGATGCAAGCGT	
Consensus	(301)	GACCC GAAAC GTTACACCAT GGACAAACCAATGAAAAATTGGGATGAGAAGCGT	
		361	420
Fenugreek	(307)	AAAGATGGCTATTTTCATCATCCTCATTCGCGGCTGGAGCAACCGAAAAGATACTTGT	
Guar-GalT1	(349)	AAGGAGTGGTTGCTGCATCATCCTTCTGTTTGGCGCCGACGACGCGATAAGATTCTCCTG	
Guar-GalT2	(322)	GAGGAGTGGCTGCGGCTTCATCCTTCTTCGCGCCCGGAGCGAGAGAACGAGTTTGTG	
Consensus	(361)	AAGGAGTGGCTGCTGCATCATCCTT TCGCGCCCGGAGCAAGCGAAAAGATTCT GTG	
		421	480
Fenugreek	(367)	ATAACGGGTTTACAGCCGACAAAGTGTGACAACCCCATCGGABACCACCTTTTACTAAGG	
Guar-GalT1	(409)	GTGACAGGTTCTCAGCCGAAACGGTGCCATAACCCGATCGGCGACCACTCTGTGTGGG	
Guar-GalT2	(382)	GTGACCGGATCGTAGCCGACCGTGCCGGAATCCCATCGGCGACCACTTGTGTGTACCG	
Consensus	(421)	GTGAC GGTTC CAGCCGACAC GTGCCA AACCCCATCGGCGACCACT CTGTGTACCG	
		481	540
Fenugreek	(427)	TTCTATAAAACAAGGTTGATTATTGTCGTATACACAACACGACATAATCTACAACAAT	
Guar-GalT1	(469)	TTTTCAAGAACAAGGTGGATTACTGCGGGCTGCACAACTACGACATAATTTACAACAAC	
Guar-GalT2	(442)	TTTTTTAAGAACAAGGTGGATTACTGTGCGTTACACGGGTACGATATCGTGTACAACAAT	
Consensus	(481)	TTTTTTAAGAACAAGGTGGATTACTGTGCG TACACAACCTACGACATAAT TACAACAAT	
		541	600
Fenugreek	(487)	GCATTGTTGCACCCAAAATGGACTCTTACTGGGCCAAGTATCCTATGGTTCCGGCCGCA	
Guar-GalT1	(529)	GCGCTTCTGCATCCTAAAATGAACCTCTTATGGGCCAAGTATCCAGTGATTCCGGCCGCG	
Guar-GalT2	(502)	GCATTGTTACACCCGAAAATGTTACGTTATTGGGCCAAGTACCGGTGGTGGCGCCGCG	
Consensus	(541)	GCATTGTTGCACCC AAAATG ACTCTTATTGGGCCAAGTATCC GTGGTTCCGGCCGCG	
		601	660
Fenugreek	(547)	ATGTTGGCCCATCCGGAAGTAGAATGCATATGCTGGGTCGACTCTGATGCCATCTTTACG	
Guar-GalT1	(589)	ATGATGGCCCATCCGGAAGTGGAGTGGCTCTGGTGGGTGSACTCGGACGCGGTTTCAGG	
Guar-GalT2	(562)	ATGATGGCCCATCCGGAAGCCGAGTGGATCTGGTGGGTCGACTCGGACGCGTGTTCACC	
Consensus	(601)	ATGATGGCCCATCCGGAAGT GAGTGGAT TGGTGGGTCGACTCGGACGCG T TTCACC	
		661	720
Fenugreek	(607)	GATATGGAATTCAAGTTACCGTTATGGCGTTACAAGGATCACAACCTTGTGATTCATGGT	
Guar-GalT1	(649)	GACATGGAGTTCAAGCTTCCGTTAAAGCGTTATAAGAACCAACATCTGTGGTTACCGGT	
Guar-GalT2	(622)	GACATGGAGTTCAAACTACCAATTAGATTAATAAGGATCACAACCTCGTCGTCCATGGC	
Consensus	(661)	GACATGGAGTTCAAGCTACCGTTA AGCGTTACAAGGATCACAACCT GTGGTTTCATGGT	

FIGURE 7a (Sheet 1 of 3)

		721		780
Fenugreek	(667)	<u>TTGGGAAGAGTTGGTTAAGACAGAGCATAGTTGGACCGGGCTTAACGCGGGTGTTCCTTG</u>		
Guar-GalT1	(709)	<u>TTGGGAAGGATTGGTACGGTTGAACCATAGCTGGACCGGGCTTAACGCGGGCGTATTCTTG</u>		
Guar-GalT2	(682)	<u>TTGGGCCACCTCATCCACGAGAAACGTAGTTGGACCGGGCTCAACGCGGGCGTCTTCCTC</u>		
Consensus	(721)	TTGGGAAGA TTGGT CAG GAA CATAGTTGGACGGG CT AACGCGGGCGT TTCTTG		
		781		840
Fenugreek	(727)	<u>ATGAGGAATTGTCAATGGTGGTGGATTATGGATGTTTGGGCCAGTATGGGCCCCAAC</u>		
Guar-GalT1	(769)	<u>ATTTCGGAAATTGCCAGTGGTGGTGGACTTCATGGATGTTTGGGTGAGCATGGGCCCCACG</u>		
Guar-GalT2	(742)	<u>ATCAGAAACGTGTCAATGGTCAATGGACCTTCATAAACGAATGGGCCAGCATGGGCCCCACAA</u>		
Consensus	(781)	AT AGGAATTGTCAATGGTGGT TGA TTCATGGATGT TGGGCCAGCATGGGCCCCACA		
		841		900
Fenugreek	(787)	<u>AGCCCGGAATACGAGAAATGGGGGGAGAGACTTAGAGAAACTTTAAGACAAAGTGGTA</u>		
Guar-GalT1	(829)	<u>ACTCCGGAATACGAGAAATGGGGGGAGAGGTTCAGAGAGACATTCAAGGACAAAGTGGT</u>		
Guar-GalT2	(802)	<u>ACTCCGAATACGAGAAATGGGGTCAAGCCCTAAGTCAACTTTCAAGACAAATCTTC</u>		
Consensus	(841)	ACTCCGGAATACGAGAAATGGGGGGAGAG CT AGAGAAACTTTCAAGGACAAAGTG T		
		901		960
Fenugreek	(847)	<u>CTGATTTCAGATGATCAGACGGCGCTGCTTACTTGATCGCGATGGGAGAG---GGACAAG</u>		
Guar-GalT1	(889)	<u>CCTGATTTCGACGATCAGACGGCGCTGCTTACCTGATCGCGACGGATAATAAGGACACG</u>		
Guar-GalT2	(862)	<u>CTCGAGTTCAGACGATCAGACGGCGCTGCTTACCTGATCGCGATCGAGAG---AGGAAAA</u>		
Consensus	(901)	CCTGATTTCAGACGATCAGACGGCGCT GCTTACCTGATCGCGATGGA AA GGACAAG		
		961		1020
Fenugreek	(904)	<u>TGGACAAGAAGATCTATATGGAGAATGAGTATTATTTGAAGGGTATTTGGTTAGAGATT</u>		
Guar-GalT1	(949)	<u>TTGGAGGGAGAAGATCTTCTTGGAGGCGAGTACTACTTCGAAGGGTACTTGGTTCGAGATC</u>		
Guar-GalT2	(919)	<u>TTGGCCGGAAGAAGATTTACTTAGAGAATCGTATTATTTTGAAGGGTACTTGGGAAGAAATC</u>		
Consensus	(961)	TGGACGGAGAAGATCTACTTGGAGAACGAGTATTATTTTGAAGGGTACTGG TAGAGATC		
		1021		1080
Fenugreek	(964)	<u>TCAAAGATGATGATAAATGGGTGAGAGATATGATGAGATAGAAAAGAGTGGGAAGGG</u>		
Guar-GalT1	(1009)	<u>GTGAAGACGTACGAGAACTAAGCGAGAGCTATGATGAGCTGGACAGGAAGGTGGAAGGG</u>		
Guar-GalT2	(979)	<u>GTCCGAACATTCGAGAAATAAGCAAGAAATCAACAGAGATCGAAACGGGGGTGCGCAGG</u>		
Consensus	(1021)	GT AAGACGTACGAGAA ATAAGCGAGAGATATGATGAGAT GAAA GAGGGTGGGAAGGG		
		1081		1140
Fenugreek	(1024)	<u>TTAAGGAGGAGGCATGCCAGGAAAGTGAGTGAACTTATGCTGAAATGAGAGAGGAGTAT</u>		
Guar-GalT1	(1069)	<u>TTGAGGAGGAGGCATGCCGGAAGAGGTGAGCGAGAAATACGGTTCGATGAGGGAGGAGTAT</u>		
Guar-GalT2	(1039)	<u>TTAAGAAAGGCCTCACGCGGAGAAAGTGAGTGAACTTACGGTCAAGAGAGGGAAGATAT</u>		
Consensus	(1081)	TTAAGGAGGAGGCATGCCGGAAGTGAGTGAA TTACGGTGAATGAGGAGGAGTAT		
		1141		1200
Fenugreek	(1084)	<u>GTTAAGAAATTTACGGGATAT-----CAGAAGACCTTTTATTACACATTTTACA</u>		
Guar-GalT1	(1129)	<u>CTGAAGGACA-----ACAA-----CAGGAGGCCCTTTATCAGCACTTTACT</u>		
Guar-GalT2	(1099)	<u>TTAACTCGGAAGCGTAAACGGTAAAGGAAGCTGGAGACGGCCCTTGTGACGCACTTCAG</u>		
Consensus	(1141)	T AAGGA AGG ACA GAGAAGGCC TTTAT ACGCACTTTAC		
		1201		1260
Fenugreek	(1132)	<u>GGGTGCCAACCTTGTAATGGTCAATATAATCCAAATATATGCTGCAGATGATTGCTGGAAT</u>		
Guar-GalT1	(1171)	<u>GGGTGTCAACCTTGTAATGGCCACATAATCCCTGTATAATGCTAATGATTGCTGGAAAT</u>		
Guar-GalT2	(1159)	<u>GGGTGTCAACCTTGTAAGCGGAATATAATCCGTATGTATAACGCCGAAGATTGTGGAACT</u>		
Consensus	(1201)	GGGTGTCAACCTTGTAATGG CA CATAATCCTAT TATAATGC GATGATTGCTGGAAT		
		1261		1320
Fenugreek	(1192)	<u>GGCATGGAGAGCTCTCAATTTTCTGATAATCAGGTGTTGCGCAAGTTTGGTTTCATT</u>		
Guar-GalT1	(1231)	<u>GGCATGGAGAGGCTCTTAATTTTCGCTGATAATCAAACTTGGCTACTTACCGTTATCAC</u>		
Guar-GalT2	(1219)	<u>GGAAATGCGTAAGCCCTTAATTTTCGCTGATAATCAGGTGATGCGTAAATATGGTTTCGTA</u>		
Consensus	(1261)	GGCATGGAGAGCTCTTAATTTTCGCTGATAATCAGGTGTTGCGTAA TATGGTTTC T		
		1321		1380
Fenugreek	(1252)	<u>CATCCAAATCTATTCGATAAGTCTGTTTCTCCATTACCAATTTGGATA-CCCCGCTGCATC</u>		
Guar-GalT1	(1291)	<u>CGTCAAAATTTACTCGTCAAGTCTGTTTCACCTTACCTTTTGGTTA-CCGTCTGCATA</u>		
Guar-GalT2	(1279)	<u>CACCCGGATGTACTACATAATTCCTTTCGCCGATTCGGTTTGATTATCCCCGTAACCGG</u>		
Consensus	(1321)	CATCCAAAT TACT GATAAGTCTGTTTC CC TTACC TTTGGTTA CCCCCTGCATC		
		1381		1440
Fenugreek	(1311)	<u>ACCATATAATA-TATTATAACCTGCAGGGGTG--AATTATAATAG-TAATTGTTATGATGA</u>		
Guar-GalT1	(1350)	<u>A-----TAATG-TACTACTAC-TG-----ATAACGACAG-TTATT-TAAATTTA</u>		
Guar-GalT2	(1339)	<u>TCAGGTAATAATCATATTTAATGGGAATCTAATTATGTTGACCTCTGGCTACTCAGATTCT</u>		
Consensus	(1381)	AC TAATA TA TATTAC TG A A AAT ATGACAG T ATT TTAAGATTA		
		1441		1500
Fenugreek	(1367)	<u>TTCTTCTGTCAATAATAATCAAAATAATGAAGGTGGTGTGATGATTAGC-----</u>		
Guar-GalT1	(1391)	<u>TTATAC-GAAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA</u>		
Guar-GalT2	(1399)	<u>TTCCATGCTGTCTGTAAAGTACTACTACTACTAGTATTAATTTCTTAGTGTATATTTTAT</u>		
Consensus	(1441)	TTCTTCTGT AA AAAAAATAAATAAT GT T A T TTAG		

FIGURE 7b (Sheet 2 of 3)

		1501		1560
Fenugreek	(1416)	-----		
Guar-GalT1	(1418)	-----		
Guar-GalT2	(1459)	AATATTTTATTGTATATTTTCTGGCGTTTGCATATATAGTATCGTGTGGAGTAGTATT		
Consensus	(1501)			
		1561		1620
Fenugreek	(1416)	-----		
Guar-GalT1	(1418)	-----		
Guar-GalT2	(1519)	TAATTATGCATAAGTGAAGGGATAATTTTATTCTTTTCGAATCCCTAAAAAAAAAAAAA		
Consensus	(1561)			
		1621	1651	
Fenugreek	(1416)	-----		
Guar-GalT1	(1418)	-----		
Guar-GalT2	(1579)	AAAAAAAAAAAAAAAAAAAAAAAAAACT		
Consensus	(1621)			

FIGURE 7c (Sheet 3 of 3)

	1	60
Fenugreek-GalT	(1) ATKFG-SKN-KSSPWLSNGCIFLLGAMSALLMIWGLNSHIAPIPNNSPKFNSFTTKLKSL	
Guar-GalT1	(1) MAKFG-SRN-KSPKHSNGCCFLGAFATALLLLWGLCSFIPIPHNDPKLNSVATSLRSL	
Guar-GalT2	(1) MAKSSNSRNKISHVNLSGGLFLACAFSAFLIVWGFSSFTTPIPNETPTPELSVNSHQN	
Consensus	(1) MAKFG SRN KS WLSNGCIFLLGAFSALLIIWGL SFI PIPNS PKFNSLST LKSL	
	61	120
Fenugreek-GalT	(59) NFTTN-TNFAGPDLHDSBOKTFYDDPETCYTMMDKPMKNWDEKRKEWLFHHPSFAGAT	
Guar-GalT1	(59) NFPKNPAATLPPNLOHDPDPTTFYDDPETSYT-MDKPMKNWDEKRKEWLLHHPSGAAAR	
Guar-GalT2	(61) DAVSR---GCPDFRFDPPDRTFYDDPEMCGYT-IDTTVRDWDAREEWLRHPSFAACAR	
Consensus	(61) NF SN AGPDL HDPDKTFYDDPET YT MDKPMKNWDEKRKEWL HHPSPAAGAR	
	121	180
Fenugreek-GalT	(118) EKILVITGSQPTKCDNPIGDHLRLRFYKNKVDYCRINHNDIINYNALLHPKMDSYWAKYP	
Guar-GalT1	(118) DKILVITGSQPKRCHNPIGDHLRLRFKNKVDYCRILHNYDIIYNYNALLHPKMNSYWAKYP	
Guar-GalT2	(116) ERVLVITGSQAPCRNPIGDHLRLRFKNKVDYCRILHGYDIVYNALLHPKMTYWAKYP	
Consensus	(121) EKILVITGSQP KC NPIGDHLRLRFKNKVDYCRILHNYDIIYNYNALLHPKM SYWAKYP	
	181	240
Fenugreek-GalT	(178) MVRAAMLAHPEVEWIHWVSDAIFTDMEFKLPLWRYKDHNLVHGWEEVLKTEHSWTGLN	
Guar-GalT1	(178) VIRAAMAHPEVEWVWVSDAVFTDMEFKLPLKRYKNHNLVHGWEEVLRLNHSWTGLN	
Guar-GalT2	(176) VVRAAMAHPEAEWIHWVSDALFTDMFVKLPLDHYKDHNLVHGWAAHLTHEKRSWTGLN	
Consensus	(181) VVRAAMAHPEVEWIHWVSDAIFTDMEFKLPL RYKDHNLVHGWEE LK HSWTGLN	
	241	300
Fenugreek-GalT	(238) AGVFLMRNCQWSLDFMDVWASMGPNSEPEYKWERLRETFKTKVVRDSDDDQALAYLIAM	
Guar-GalT1	(238) AGVFLIRNCQWSLEFMDVWVSMGPQTEPEYKWERLRETFKDKVLPSDDQALAYLIAT	
Guar-GalT2	(236) AGVFLIRNCQWSLDFINWASMGPTENYEKGQTLKSTFKDKFFPESDDQGLAYLIAT	
Consensus	(241) AGVFLIRNCQWSLDFMDVWASMGPTPEYKWERLRETFKDKVLPSDDQALAYLIAT	
	301	360
Fenugreek-GalT	(298) G-EDKATTKTYMENEFYFEGYWLEISKMYDKMGERLDEIEKRVEGLRRRHAEKVSEKYGE	
Guar-GalT1	(298) DNKDTWREKIFLESEYFEGYWLEIVKTYENISERNDEVERKVEGLRRRHAEKVSEKYGA	
Guar-GalT2	(296) E-KKKWADKTYLENSYFEGYWEEIVGTENISKYNEIETGVRRRLRRRHAEKVSEKYGE	
Consensus	(301) D KDKW DKTYLENEYYFEGYWLEIVKTYENISERYDEIEKKVEGLRRRHAEKVSEKYGE	
	361	420
Fenugreek-GalT	(357) MREEYVKNLG---DMRRPFIHTFTGCQPCNGHHNPIYAADDWCNMGERALNFADNQVLR	
Guar-GalT1	(358) MREEYLNKDNK-----RRPFIHTFTGCQPCNGHHNPAZNANDWCNMGERALNFADNQVLR	
Guar-GalT2	(355) EREKYLTEAGNGKGSWRPFPVTHFTGCQPCSGKYNAMYNAEDWCNMGKALNFADNQVLR	
Consensus	(361) MREEYLNK G RRPFIHTFTGCQPCNGHHNPIYNADDWCNMGERALNFADNQVLR	
	421	451
Fenugreek-GalT	(413) KFGFIHPNLLDKSVSHLPFCYHAASP-----	
Guar-GalT1	(412) TYGYHRQNLDDKSVSHLPFCYPAA-----	
Guar-GalT2	(415) KYGFVHPDVLNDSVSPIPFDYERNRSGNNHI	
Consensus	(421) KYGFHPNLLDKSVSPLPFGYPAA	

FIGURE 8

	1	60
AtCesA1	(1)	MEASAGLVAGSYRRNELVIRHESDGG--TKPLKNMNGQICQICGDDVGLAETGDVFFVAC
ZmCesA1	(1)	MAANKGMVAGSHNRNEFVMIRHDGDVPGSAKPTKSANGQVCQICGDSVGVSATGDVFFVAC
GhCesA1	(1)	-----MMESGVPVCHTCGEHVLNVNGEPFVAC
PtCesA	(1)	-----MMESGAPICHTCGEQVGHDAENGELFVAC
CtManS	(1)	-----
AtCslA9	(1)	-----
AtCslB1	(1)	-----
AtCslC4	(1)	-----
AtCslD1	(1)	-----MASSPPKKTLSQSSSLRPPQAVKFGRRTSSEGRIVLSLRDDMDVSGDYSQGN
AtCslE1	(1)	-----
AtCslG1	(1)	-----
Consensus	(1)	-----
	61	120
AtCesA1	(59)	NECAFPVCRPCYERKDGTCQCPQCKTRFRRHRGSPRVEGDEDEDVDDIENEFNYAQG
ZmCesA1	(61)	NECAFPVCRPCYERKEGNQCCPQCKTRYKRQKGSPRVHGDEDEDVDDLNEFNKYQG
GhCesA1	(29)	HECNFPICKSCFEYDLKEGRKACLRGSPY-----D-ENLLDDVEK-ATGDQS
PtCesA	(29)	HECSYPMCKSCFEFEINEGRKVCRLRGSPY-----D-ENLLDDVEKKGSGNQS
CtManS	(1)	-----
AtCslA9	(1)	-----
AtCslB1	(1)	-----
AtCslC4	(1)	-----
AtCslD1	(55)	DYINYTVLMPPTPDNQAGSSGSTSESKGDNRRGGG---GGDGPKMGNKLERRLSVMKS
AtCslE1	(1)	-----
AtCslG1	(1)	-----
Consensus	(61)	-----
	121	180
AtCesA1	(119)	ANKAR---HQRHGEFSSSSSRHESQP-IPLLTHGHTVSGEIRTPDTQSVRTTSGPLGPSD
ZmCesA1	(121)	SGKGPEWQLQGDDADLSSSARHEPHHRIPRLTSGQQISGEIPDASPDRHSIRS--P----
GhCesA1	(75)	TMAAHLN---KSQDVGIHARHIS-----S-----VSTLDSEMA-----
PtCesA	(76)	TMASHLN---DSQDVGIHARHIS-----S-----VSTVDSEMN-----
CtManS	(1)	-----
AtCslA9	(1)	-----
AtCslB1	(1)	-----
AtCslC4	(1)	-----
AtCslD1	(111)	NNKSMLLRSQTDGDFDHNRLWFESK-----
AtCslE1	(1)	-----
AtCslG1	(1)	-----
Consensus	(121)	-----
	181	240
AtCesA1	(175)	RNAISSPYIDPRQVPVRIVDPSKDLNSYGLGNVDWKERVEGWKLQEKNNMLQMTGKYHE
ZmCesA1	(175)	----TSSYVDPSVPVPRIVDPSKDLNSYGLNSVDWKERVESWRVKQDKNNMQVTNKYPE
GhCesA1	(105)	-----EDN-----GNSIWKNRVESWKEKKNNKKKKPATTKVER
PtCesA	(106)	-----DEY-----GNPIWKNNRVKSKDKENKKKKRSPKAETE
CtManS	(1)	-----
AtCslA9	(1)	-----
AtCslB1	(1)	-----
AtCslC4	(1)	-----
AtCslD1	(135)	-----GKYGIGNAFWSEEDDTYDGGVSKS--
AtCslE1	(1)	-----
AtCslG1	(1)	-----
Consensus	(181)	-----
	241	300
AtCesA1	(235)	GKGGEIEGTGSNGEELQMAADDTRLPMSSRVVPIPSRLTPYRVVILRLIILCFFLQYRTT
ZmCesA1	(231)	ARGGDMEGTGSNGEDMQMVDDARLPLSRIVPISSNQLNLRVVILRLIILCFFFOYRVVS
GhCesA1	(137)	EAEIPPEQQ---MEDKPADASQPLSTIIPKSRILAPYRTVILRLIILGLFFHYRYVT
PtCesA	(138)	PAQVPTEQQ---MEEKPSASEPLSIVYPIPRNKLTPIYRAVILRLIILGLFFHYRYVT
CtManS	(1)	-----
AtCslA9	(1)	-----
AtCslB1	(1)	-----
AtCslC4	(1)	-----MAPNSVAVTMEKPDNFSLEINGSDPSSFDPKRKSTSPKQFSWFLLLKAH
AtCslD1	(159)	-----DFLDKPKWKPLTRKVQIPAKILSPYRLILVIRLVIVFFFLWRRIT
AtCslE1	(1)	-----MVNKDDRIRPVHEADGEPLFETRRRTGRVIAIRFFSASVFCICLIWFYRIG
AtCslG1	(1)	-----METHRKNSVVGNIHHTCHPCRRITPIYRIATFHTCGIALMYHHVH
Consensus	(241)	D S L YR II I L F YRI

FIGURE 9a (Sheet 1 of 4)

	301		360
AtCesA1	(295)	HPVKN---AYPLWLTSVCEIWFAFSWLLDQFPKWYPINRETYLDRLAIRYDRDGEP--	
ZmCesA1	(291)	HPVRD---AYGLWLVSVICEVWFALSWLLDQFPKWYPINRETYLDRLAIRYDRDGEP--	
GhCesA1	(193)	NPVDS---AFGLWLTSVCEIWFAFSWLLDQFPKWYPVNRRETYIDRLSARYEREGERP--	
PtCesA	(194)	NPVDS---AFGLWLTSVCEIWFAFSWLLDQFPKWVNRRETYIERLSARYEREGERP--	
CtManS	(1)	-----	
AtCslA9	(1)	-----	
AtCslB1	(1)	--MNQ---NNSVWVVAFLCESEFSFIWLLITSIKWSPASYKSYPERLDERVH-----	
AtCslC4	(51)	RLISC---LSWLVS SVKKRIAFSAKNINEEEDPKSRGKQMYRFKACLVISIIALSI--	
AtCslD1	(203)	NPNE---AMWLWGLSIVCEIWFAFSWLLDILPKLNPNRATDLAALHDKFEQSPSPNP	
AtCslE1	(53)	EIGDNRTVLDRLIWFVMFIVEIWFGLYVVTQSSRWNPVWRFPFSDRLSRRYG-----	
AtCslG1	(47)	SLVTAN---NTLITCLLLSLDIVLAFMWATTTSLRLNPFVHRTECPKYAAKPE-----	
Consensus	(301)	V LW SVCEIWF AF WLLD PKW PVNR TYIDRLA RYE	
	361		420
AtCesA1	(349)	---SQLVPVDVFFVSTVDPDKKEPPLVTANTVLSLSDYDPVDKVCYVSDDGSAMLTFFESL	
ZmCesA1	(345)	---SQLAPIDVFFVSTVDPDKKEPPLVTANTVLSLSDYDPVDKVCYVSDDGSAMLTFFESL	
GhCesA1	(247)	---DELAADVDFVSTVDPDKKEPPLVTANTVLSLSDYDPVDKVCYVSDDGSAMLTFFESL	
PtCesA	(248)	---SQLAGVDFVSTVDPDKKEPPLVTANTVLSLSDYDPVDKVCYVSDDGSAMLTFFESL	
CtManS	(1)	-----MRNLIFEPEPIGNSSSLRYAWQSIRAPVILPLKLAVIVCSVMSIM	
AtCslA9	(1)	-----MEIGDTTSVIPDSFMGYRDDITMQMSVLDQIRAPLIVPALRLGVYICLTMSVM	
AtCslB1	(48)	---DLPSVDMFVTADDPVREPPILVANTVLSLAVNYPANKLACYVSDDGCPLTVFSL	
AtCslC4	(105)	---EIVAHFKKWNLDITINRPSWEVYGLVIEWSYMAWLSERSDYIAPLVISLSRFTVLFIL	
AtCslD1	(259)	TGRSDLPGVDFVSTADPEKEPPLVTANTVLSLSDYDPIEKL SAYTSDDGGAITLTFEM	
AtCslE1	(106)	---SDLPRLDVFCVCTADDPVIEPPLLVVNTVLSVLTALDYPPKLA VYLSDDGGSELTFFAL	
AtCslG1	(97)	---DFPKLDVFCVCTADDPYKEPPMMVNTALSVMAYEYPSDKISVYVSDDGGSELTFFAL	
Consensus	(361)	L VDFVSTVDPLKEPPLI ANTVLSILAVDYP DKIS YVSDDG A LTF SL	
	421		480
AtCesA1	(406)	SETAEFAKKWVPFCKKFNIEPRAPPEFYFAQKIDYLDKDIQ--PSFVKERRAMKREYEEFK	
ZmCesA1	(402)	SETAEFAKKWVPFCKKFNIEPRAPPEFYFAQKIDYLDKDIQ--PSFVKERRAMKREYEEFK	
GhCesA1	(304)	VETADFARKWVPFCKKFNIEPRAPPEFYFAQKIDYLDKDIQ--PSFVKERRAMKREYEEFK	
PtCesA	(305)	VETAEFAKKWVPFCKKFNIEPRAPPEFYFAQKIDYLDKDIQ--PSFVKERRAMKREYEEFK	
CtManS	(50)	LFVERVAMAAVILIVFLRKKRYTKYNLEAMKQKLEKSK--YPMVLIQIPMYKEVYK	
AtCslA9	(55)	LFVERVYMGIVISLVFLGRKPKDKREKYEPIKDDIELGNSA--YPMVLIQIPMFNEREVYQ	
AtCslB1	(104)	KEASKFAKIVWVPFCKKYNIKVRAFPFYFLNPPAATSS----EFSKDWEITKREYEKLS	
AtCslC4	(162)	QSLDLVLVLCGCFWIKKK---IEPKLTEESIDLEDPS--FPMVLIQIPMCNEREVYE	
AtCslD1	(319)	AEAVRFAEYWVPFCKKHDIEPRNPDSYFSIKKDPKTKNKR--QDFVKDRRWIKREYDEEK	
AtCslE1	(163)	TEAAEFATWVPFCKKFNVEPTSPAAYLSSKANCLDSAAE--EVAKLYREMAAR--IETA	
AtCslG1	(153)	IEAAKFSKQWLPFCKKNNVQDRSPEVYFSSESHSRSDAENLKTNTLKCEVEQMMYEDMK	
Consensus	(421)	E ARFAK WVPFCKKF IEPRAPPEFYFS K D L D FVKER MKREYEEYK	
	481		540
AtCesA1	(464)	VRINALVAKAOKIPEEG-----WTMQDGTWPWPGNN	
ZmCesA1	(460)	VRINALVAKAOKVPEEG-----WTMADGTAWPGNN	
GhCesA1	(362)	VRINALVAKAOKTPDEG-----WTMQDGTWPWPGNN	
PtCesA	(363)	VRINALVAKAOKTPDEG-----WTMQDGTWPWPGNN	
CtManS	(108)	LSIGAVCGLSWPADRFI-----VQVLDDSTNP--	
AtCslA9	(114)	LSIGAACGLSWPSDRIV-----IQVLDDSTDP--	
AtCslB1	(159)	RRVEDATGDSHWLDAED-----DFEDFSNTK	
AtCslC4	(216)	QSIGAASQLDWPKDRIL-----IQVLDDSDDP--	
AtCslD1	(377)	VRINGLPEQIKKRAEQFNMREELKEKRIAREKNGGVLPDPGVEVVKATWMADGTHWPGTW	
AtCslE1	(219)	ARLGRIPPEARVKYGDG-----FSQWDADA	
AtCslG1	(213)	SRVEHVVESGKVETAFIT-----CDQFRGVFDLWTDKF	
Consensus	(481)	VRI AL A A E M D T WPG	
	541		600
AtCesA1	(494)	TR-----DHPGMIQ-VFLGHSGGLDTDGNE-----LPRLIVVSREKRPGE	
ZmCesA1	(490)	PR-----DHPGMIQ-VFLGHSGGLDTDGNE-----LPRLIVVSREKRPGE	
GhCesA1	(392)	PR-----DHPGMIQ-VFLGYSGARDIEGNE-----LPRLIVVSREKRPGE	
PtCesA	(393)	TR-----DHPGHDSGLPWEILGARDIEGNE-----LPRLIVVSREKRPGE	
CtManS	(135)	-----VLRELVEMECQKWIQK-----V-NVKYENRNRNGY	
AtCslA9	(141)	-----TIKDLVEMECSRWASKG-----VNKYEIRDNNGY	
AtCslB1	(185)	PN-----DHSTIVK-VVWENKGGVGVEN-----EVPHFVYISREKRPNY	
AtCslC4	(243)	-----NLQLLIKEVSVWAEKG-----V-NIIVRHRLIRTGY	
AtCslD1	(437)	FEPKPDHSGDHAQTLQIMSKVPDLEPVMGGPNEGALDFTGIDIRVPMFAVVSREKRPGE	
AtCslE1	(244)	TRR-----NHGTILQVLVDGREG-----N-TIAIPTLYLSREKRPQH	
AtCslG1	(246)	SR-----HDHPTILQVLQNSQTD---MDNTR-----KYIMPNIIVVSREKSKVS	
Consensus	(541)	R DH IIQ L G DG LP LVVVSREKRPGE	

FIGURE 9b (Sheet 2 of 4)

		601		660		
AtCesA1	(533)	QHHKKAGAMNALIRVSAVLTNGAYLLNVDCDHYFNNSKAIKEAMCFMMDPA	-	IGKKCCYV		
ZmCesA1	(529)	QHHKKAGAMNALIRVSAVLTNGAYLLNVDCDHYFNSSKALREAMCFMMDPA	-	LGRKTCYV		
GhCesA1	(431)	QHHKKAGAENALVRVSAVLTNAPFLLNLDCHYVNNSKAVREAMCFMMDPQ	-	WGRDVCYV		
PtCesA	(433)	QHHKKAGAENALVRVSAVLTNAPYLLNVDCDHYVNNSKAVREAMCILMDPQ	-	VGRDVCYV		
CtManS	(166)	KAGALKEGLEKQY	----	VEDCEPVAIFDADFQPDADFLWNTIPYLLNPK	-	LGLVQARW
AtCslA9	(172)	KAGALKEGMKKS	Y----	VKSCDYVAIFDADFQPEADFLWRTVPYLLHNPK	-	LALVQARW
AtCslB1	(223)	LHHYKAGAMNFLVRVSGMLTNAPYMLNVDCDHYANEDVVRQAMC	IF	LQKSMNSNHCAFV		
AtCslC4	(274)	KAGNLKSAMTCDY	----	VKDYEFTVIFDADFTPNPDLKKTVPHEKGNPE	-	LGLVQARW
AtCslD1	(497)	DHNKAGAMNGMVRASAILSNAGFILNLDCHYIYNSKAIKEGMCFFMDR	-	GGDRICYT		
AtCslE1	(281)	HHNFKAGAMNALIRVSSKITCGKITLNLCDMYANNSKSTRDAICILDEK	-	EGKEIAFV		
AtCslG1	(287)	PHHFKAGALNTLIRVSGVMTNSPIILTLCDMYSNDPATLVRAICYLTD	P	EIKSGLGYV		
Consensus	(601)	HH KAGAMNALVRVSAVLTNG YILNLD CD Y N SKAVREAMCFM DP LG		AYV		
		661		720		
AtCesA1	(592)	QFPQRF DGI D YAN N VFFDINMKGLDGIQGPVYVGTGCVF	R ALY			
ZmCesA1	(588)	QFPQRF DGI D YAN N VFFDINMKGLDGIQGPVYVGTGCVF	R ALY			
GhCesA1	(490)	QFPQRF DGI D YAN N VFFDINMKGLDGIQGPVYVGTGCVF	R ALY			
PtCesA	(492)	QFPQRF DGI D YAN N VFFDINMKGLDGIQGPVYVGTGCVF	R ALY			
CtManS	(220)	KVNSEECMTRLQEMSLDYHFSVEQEVGSSTYSFFGNGTAGVWRIQATK	DAG-----			
AtCslA9	(226)	KVNSEECMTRLQEMSLDYHFTVEQEVGSSTYAFFGNGTAGVWRIQATK	DAG-----			
AtCslB1	(283)	QFPQEF	---Y--DSNADELTVLQSYLGRGTAGTQGPVYVGTGCVF	R ALY		
AtCslC4	(328)	SVNKNDENLTRLQINILCFHFEVEQVNGVFLNFFGNGTAGVWRIKALE	ESG-----			
AtCslD1	(555)	QFPQRFEGIDPSDRYANHNTVFFDGNMRALDGLQGPVYVGTGCMFRRY	ALYGFNPP---R			
AtCslE1	(340)	QFPQCFDNTVRNDLYGSMRVDGIDVFLGLDGNGGPLVITGCFHRRDV	ICGRKYG---			
AtCslG1	(346)	QFPQKFLGISKNDIYACENKRLFIINMVGFDGLMGPTHVITGCFHRRDV	ICGRKYG---			
Consensus	(661)	QFPQRF DGI D YAN N VFFDINMKGLDGIQGPVYVGTGCVF	R ALY			
		721		780		
AtCesA1	(652)	DLEP	---NIIIVKSCCGSRKKGKSSKKYNYEKRRGINRSDSNAPLFNME	IDEFGEGYDDE		
ZmCesA1	(648)	DLEP	---NIVIKSCCGRRK--KNKSYMDSQSRIMKRTSSAPIFNME	IEEGIEGYEDE		
GhCesA1	(550)	FPK	---SSSSSCSCCPGKKE---PKDPSELYRDAKRELDAAIFNIRE	IDN---YDEYE		
PtCesA	(552)	LRRKRDSSSCFSCCPSKKKP	---AQDPAEVYRDAKREDLNAAIFNIRE	IDN---YDEHE		
CtManS	(274)	-----				
AtCslA9	(280)	-----				
AtCslB1	(332)	-----				
AtCslC4	(382)	-----				
AtCslD1	(612)	-----				
AtCslE1	(396)	-----				
AtCslG1	(400)	-----				
Consensus	(721)	-----				
		781		840		
AtCesA1	(709)	RSILMSQRSVEKREFGQSPVFIATFMEQGG	----IPPTNPATL	LKEAIHVISCGYEDK		
ZmCesA1	(703)	RSVLMSQRKLEKREFGQSPIFIATFMTQGG	----IPPSTNPASL	LKEAIHVISCGYEDK		
GhCesA1	(601)	RSMLISQTSFEKTEGLSSVFIESTLMENG	G----VAESANPSTL	LKEAIHVISCGYEEK		
PtCesA	(606)	RSMLISQLSFEKTEGLSSVFIESTLMENG	G----VPESANSPPF	LKEAIQVIGCGYEEK		
CtManS	(274)	-----				
AtCslA9	(280)	-----				
AtCslB1	(346)	TRKYLAENLAREFGNSNEMVTSVVEALQRK	----PNPQNTLANSL	EAAQEVGHCHFEYQ		
AtCslC4	(382)	-----				
AtCslD1	(665)	NSTMTDTIPVAEYQGRPLADHMSVKNGRPPGALLLPRPPLDAPT	VAEAI	AVISCWYEDN		
AtCslE1	(396)	-----				
AtCslG1	(402)	LILPEIN--ELKPYR	-----IADKSIKAQDV	LSLAHVAGCIYEYN		
Consensus	(781)	K F		L A V C YED		
		841		900		
AtCesA1	(764)	TEWGKEIGWYGSVTEDILTGFKMHARGHISITCNPPRPAPFKGSAP	INLSDRLNQVLRNA			
ZmCesA1	(758)	TEWGKEIGWYGSVTEDILTGFKMHARGHISITCNPPRPAPFKGSAP	INLSDRLNQVLRNA			
GhCesA1	(656)	TAWGKEIGWYGSVTEDILTGFKMHARGHISITCNPPRPAPFKGSAP	INLSDRLNQVLRNA			
PtCesA	(661)	TEWGKEIGWYGSVTEDILTGFKMHARGHISITCNPPRPAPFKGSAP	INLSDRLNQVLRNA			
CtManS	(275)	-----				
AtCslA9	(280)	-----				
AtCslB1	(402)	TSWGTIGWLYESTAEADANTSIGHSRGWTSYISPKPPAFLGAMP	PGGPEAMLQORRNA			
AtCslC4	(383)	-----				
AtCslD1	(725)	TEWGDRIGWYGSVTEDVVTGYRMHNRGWSVYCITKRDAFRGTAP	INLTDRLHQVLRNA			
AtCslE1	(427)	TQWCKEMGVKYGCPVEDVITGLTIQCRGWSAYLNPEKQAF	FLGVAPTNLHQMVLQORRNA			
AtCslG1	(441)	TNWSKIGIFRYGSLVEDDYTGFMHCEGWSVFCNPKKAAFYGDSP	KCLVDLVQQRNA			
Consensus	(841)	T W G K I G W I Y G S V E D I L T G F K M H R G W S I Y C N P P R P A F K G S A P I N L S D R L N Q V L R N A				

FIGURE 9c (Sheet 3 of 4)

		901		960
AtCesA1	(824)	LGSVEILLSRHCPWIYGYHG-RLRLLERTAYINTIVYPITSIPLIAYCILPAFCLITDRF		
ZmCesA1	(818)	LGSVEILLSRHCPWIYGYNG-RLKLLERLAYINTIVYPITSIPLIAYCVLPALCLLTNKF		
GhCesA1	(716)	LGSVEIFLSRHCPWYGFGGRLKWLQRLAYINTIVYPITSIPLIAYCSLPAICLLTGKF		
PtCesA	(721)	LGSVEIFFSRHCPWYGFGGRLKWLQRLAYINTIVYPITSIPLIAYCTIPAVCLLTGKF		
CtManS	(325)	CGPANLFRKMTKEICCKR-----VPLLKRLHLIYAFFVRKIYAHWVTFFFYCIVIPAC		
AtCslA9	(331)	CGPANLFRKMAFEIMTNKN-----VTLWKKVHVIYSFFVVRKLVAHIVTFIFYCVLPAT		
AtCslB1	(462)	TGLLEVLFNKQSPITGMFCR-KIRFRQSLAYLYIFTWGLRSIPELIYCLLPAYCLLHNAA		
AtCslC4	(433)	SGPMQLFRCLCLPSIIKSK-----TSVWKKANLIFLFLLRKLIIPFYSFTLFCITLPLT		
AtCslD1	(785)	TGSVEIFFSKNNNAMEATR---RLKFLQRAYINVGIYPPTSIPLIYVYCFLPALCLFSGKF		
AtCslE1	(487)	EGDFQIMLSKYSPVWYGKG-KTSLGLILGYCCYCLWAPSSLPVLIYSVLTSLCLFKGIP		
AtCslG1	(501)	VGLPEMFSFKYSPITYGIKS--LDLLMGLGYCNSPFKPFWSIPLTVYGLLPQALISGV		
Consensus	(901)	G VEIF SKH PIWYG RLKLL LAYIN VYP TSIPLI YC LPALCLIT		
		961		1020
AtCesA1	(883)	IIPETSNYASIWFLLLFISIAVTGILELRWSGVSTEDWRNEQFWVIGGTSAHFLFAVFQ		
ZmCesA1	(877)	IIPETSNYAGMFFILLFASIFATGILELRWSGVSTEDWRNEQFWVIGGTSAHFLFAVFQ		
GhCesA1	(776)	IIPTLNLSASVLFGLFLSIIVTAVLELRWSGVSTEDLWRNEQFWVIGGVS AHFLFAVFQ		
PtCesA	(781)	IIPTLNLSASMLFLGLFISIIIVTAVLELRWSGVSTEDLWRNEQFWVIGGVS AHFLFAVFQ		
CtManS	(380)	VIVPEVNLKKOIAIYTPATITILNAVSTPRSMHLIVLWILFENVMSLHRTKAAITGLLE-		
AtCslA9	(386)	VIVPEVTVPKWGAIVIPSVITILNAVGTPRSLHLMVFWILFENVMSLHRTKATFGLLE-		
AtCslB1	(521)	LFP--KGVLGTIVTLVGMHCLYSIWEFMSLGFSVQSWFASQSFWRIKTTC ^{SWL} FPSTPDI		
AtCslC4	(487)	MFIPAEELPLWITICYVPIFISLNLPLSPKSFPPFVPPYLLFENTMSITKFNAMISGLFQ-		
AtCslD1	(842)	IVQSLDIHFLSYLCTITVTLTILISLEVKNWSGIGLEEWWRNEQFWLIGGTSAHFLAAVQ		
AtCslE1	(545)	IFPKVSSSWFIPFGYMTVAATAYSLAEFLWCGGTFRGWWEQRMWLYRRTSSFLFGMDT		
AtCslG1	(559)	VFPKASDPWFVLYLILFFGAYAQDLSDFLEGGTYRKWWDQRMIMIKGLS ^{FFF} GFIEF		
Consensus	(961)	IIP LS L IFI L ISI L LLE WSG SI WW EQFWVI GTS LFAV Q		
		1021		1080
AtCesA1	(943)	ILKVLGIDTNFTVFSKATDE--DGDEAEL-----VIFKWTALLIPPTTVI		
ZmCesA1	(937)	ILKVLGIDTNFTVFSKASDE--DGDEAEL-----VIFKWTALLIPPTTVI		
GhCesA1	(836)	FLKMLGIDTNFTVIAKAA-D--DADEGEL-----VIVKWTALLIPPTTVI		
PtCesA	(841)	FLKMLGIDTNFTVIAKAA-E--DADEGEL-----VIVKWTALLIPPTTVI		
CtManS	(439)	---AN-RVNEWVTEKLG-----NA-----MKQRNARPS---		
AtCslA9	(445)	---GGRVNEWVTEKLG-----DVKAKSATKT---		
AtCslB1	(579)	ILKVLGISKTVFIVTKTMPKTMMSGSGSEKSQREVDCPNQDSGKEFDG ^{SLY} FPGTFTI		
AtCslC4	(546)	---FG-SAYEWVTEKLG-----RS-----SESDDLAFAEKEEK		
AtCslD1	(902)	ILKVLGIDTNFTVFSKASGEDEDDIADL-----VIVKWTCLFIMPLTII		
AtCslE1	(605)	ILKVLGVSESAFAVITAKV ^{EE} EAERYKEEVMFEG-----VESPMFLVLGTIG		
AtCslG1	(619)	ILKTLNLSTPKFNVTSKANDDDEQRKRYEQEIFDFG-----TSSSMFPLTTVA		
Consensus	(1021)	ILKVLG DT F VTSKAA E F E Y K T L IP TTLL		
		1081		1140
AtCesA1	(987)	LVNLIGIVAGVSYAVNSGYQSWGPLFGKIFFALVIAHLYPFLKGLLGRQNR-----		
ZmCesA1	(981)	VIVNLVGMVAGISYAVNSGYQSWGPLFGKIFFSIVVIAHLYPFLKGLMGRQNR-----		
GhCesA1	(879)	IVNMVGVVAGFSDALNKGYEAWGPLFGKIFFSIVVIAHLYPFLKGLMGRQNR-----		
PtCesA	(884)	IIVMSG-CAGFSDALNKGYEAWGPLFGKIFFAFVIAHLYPFLKGLMGRQNL-----		
CtManS	(465)	-----RASRFRI ^{TER} IH-----		
AtCslA9	(469)	-----S-----K---KVIRFRFGDRIHV-----		
AtCslB1	(639)	LVN-LAALAGCSVGLQRRHGG-GSGLA ^{EAC} GCILVVILFLPFLKGM ^{FE} KGK-----		
AtCslC4	(576)	LHRRNS--ESGLELSKLKEQETNLVQETVKKSLGGLMRPKNKKTNMVF-----		
AtCslD1	(948)	IVNLVAIVIGASRTIYSVIPQWGLMGGIFFSLVILTHMYPPFAKGLMGRGK-----		
AtCslE1	(653)	MLNDFCFAAAVARLVSGDGD ^{LKT} MGQFVITGVLVVINWPLYKGLLRQDK-----G		
AtCslG1	(668)	IVNL ^{LA} FAVWGLYGLIFCG----GELYELMLVSEAVVNCLPIYGA ^{ML} VLRLKDDGKL ^{SKRT} C		
Consensus	(1081)	IVNLVG VAG S L G L G L WVIL LYPF KGLM R		
		1141		1192
AtCesA1	(1039)	-TPTIVIVWSVLLASIESLWVRINPFVDANPNANNFNGKGGVF-----		
ZmCesA1	(1033)	-TPTIVIVWSLTLASIESLWVKIDPPTISPTQKAALGQCGVNC-----		
GhCesA1	(931)	-TPTIVVLSVLLASVFSLVWVRINPFVSTADSTTVSQSCISIDC-----		
PtCesA	(935)	-TPTIVVLSVLLASVFSLVWVKINPFVNKVDNLVAETCISIDC-----		
CtManS	(477)	-PLEIIVGMYMLHCATYDLEFGHDHFFVYLLLOAGAFFTMGFLVGTIVPT-		
AtCslA9	(484)	--LEIGVGYMLLFVGCYDAFEGKNHYLYLFAQAIAFFIAGFGQIGTIVPNH		
AtCslB1	(688)	---YGI ^{PW} STLSKAAFLAVLVVFSVGN-----		
AtCslC4	(625)	-KKEIGLAFLLLTAAARSFLSAHGLHFYLLFQGLSFLVVGDL ^{LIGE} QIS--		
AtCslD1	(1000)	-VPTIVVWSGLVSITVSLWITISPPDDVSGSGGISV-----		
AtCslE1	(706)	KMPMSVTVKS ^{VV} LALSACTCLAFI-----		
AtCslG1	(724)	FLAGNLHVGSYCVKLLRPQVTSPLRIHNNTSGWFKRKKHNMNESV-----		
Consensus	(1141)	P IVVVWSVLLAS FSLW I FV A		

FIGURE 9d (Sheet 4 of 4)

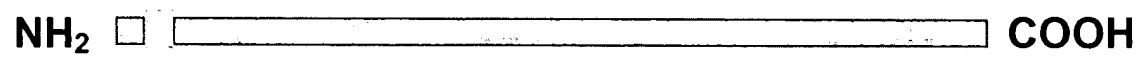
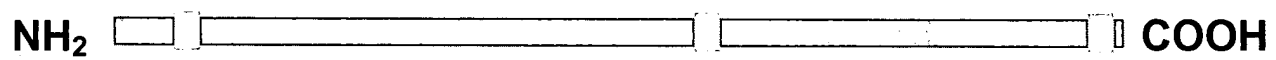


FIGURE 10

R S L 10 25 30 E SC Em



FIGURE 11

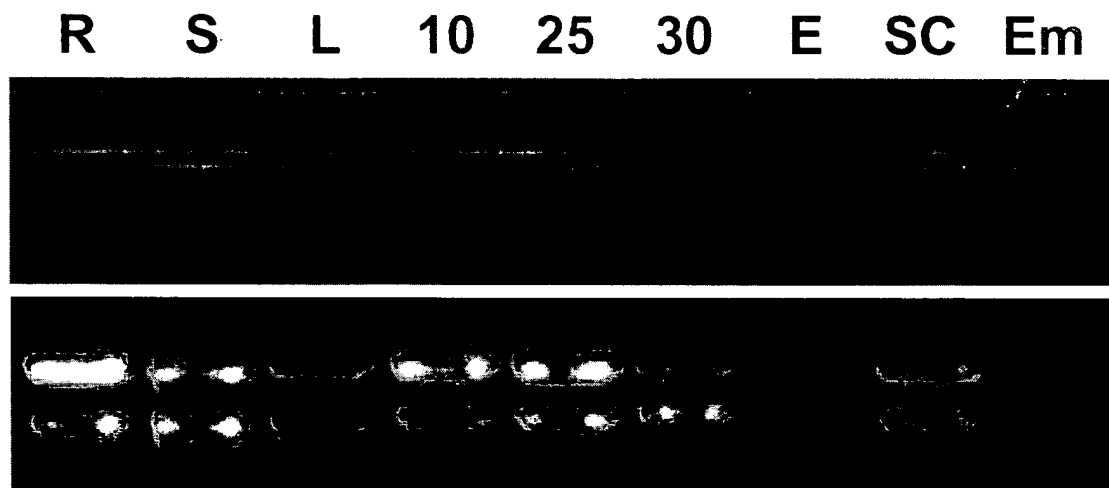


FIGURE 12A

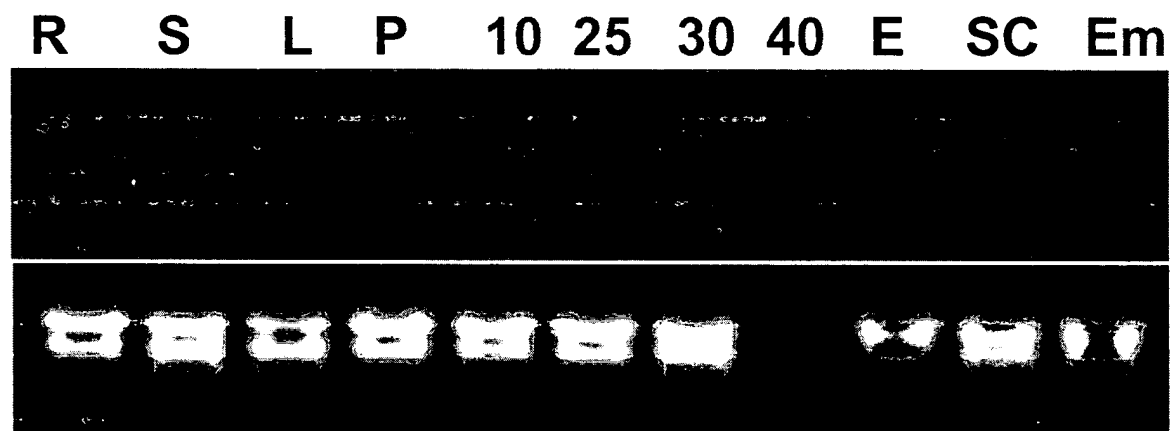


FIGURE 12B

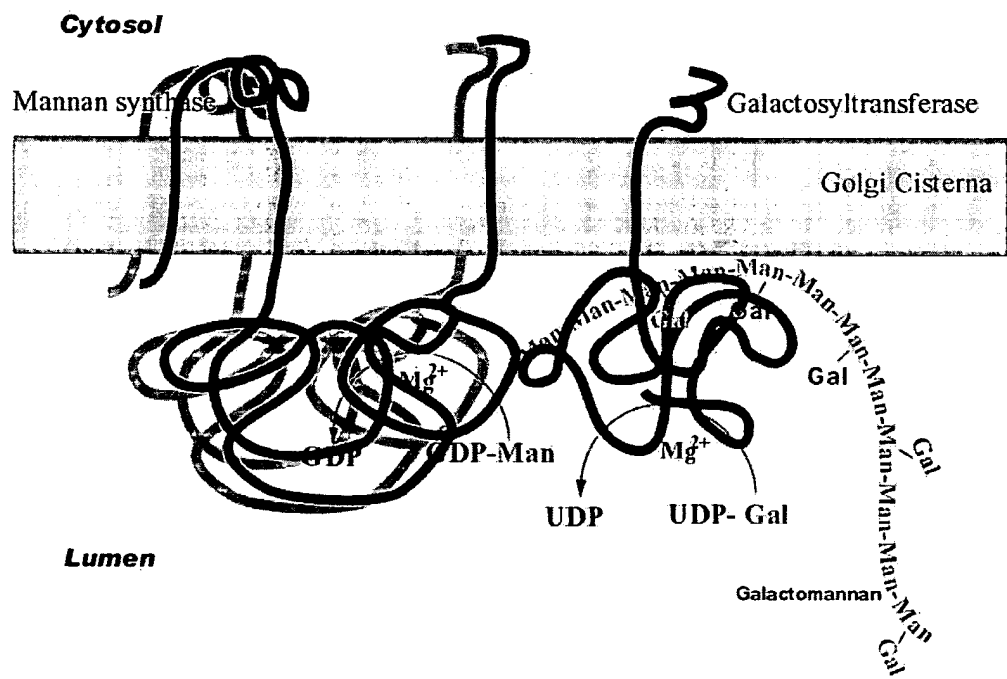


FIGURE 13

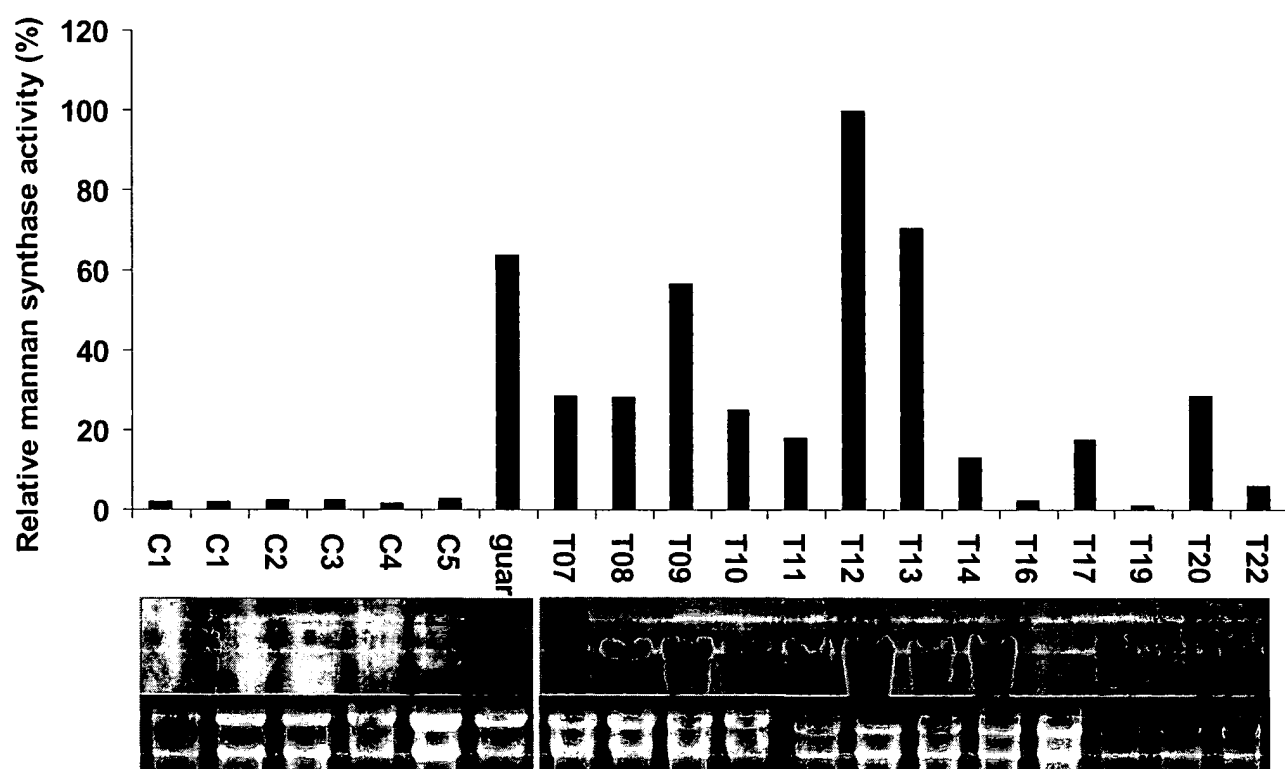


FIGURE 14

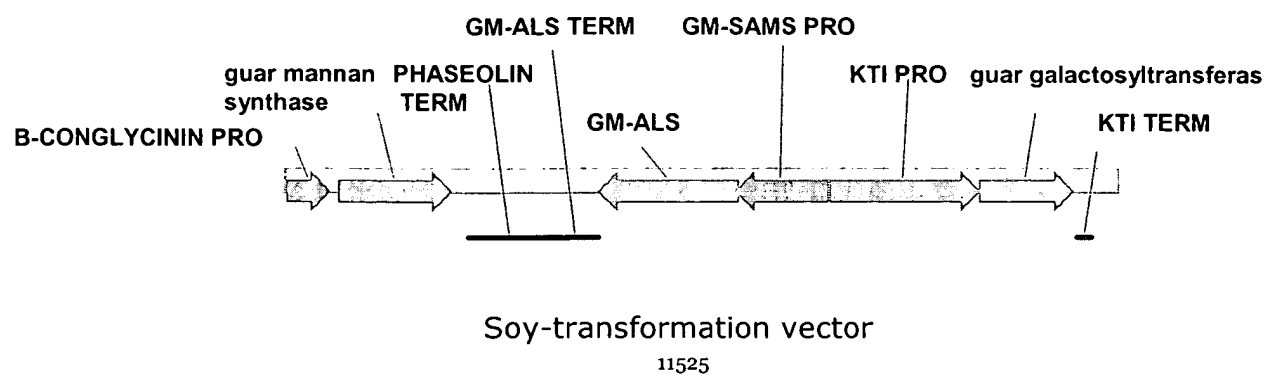


FIGURE 15

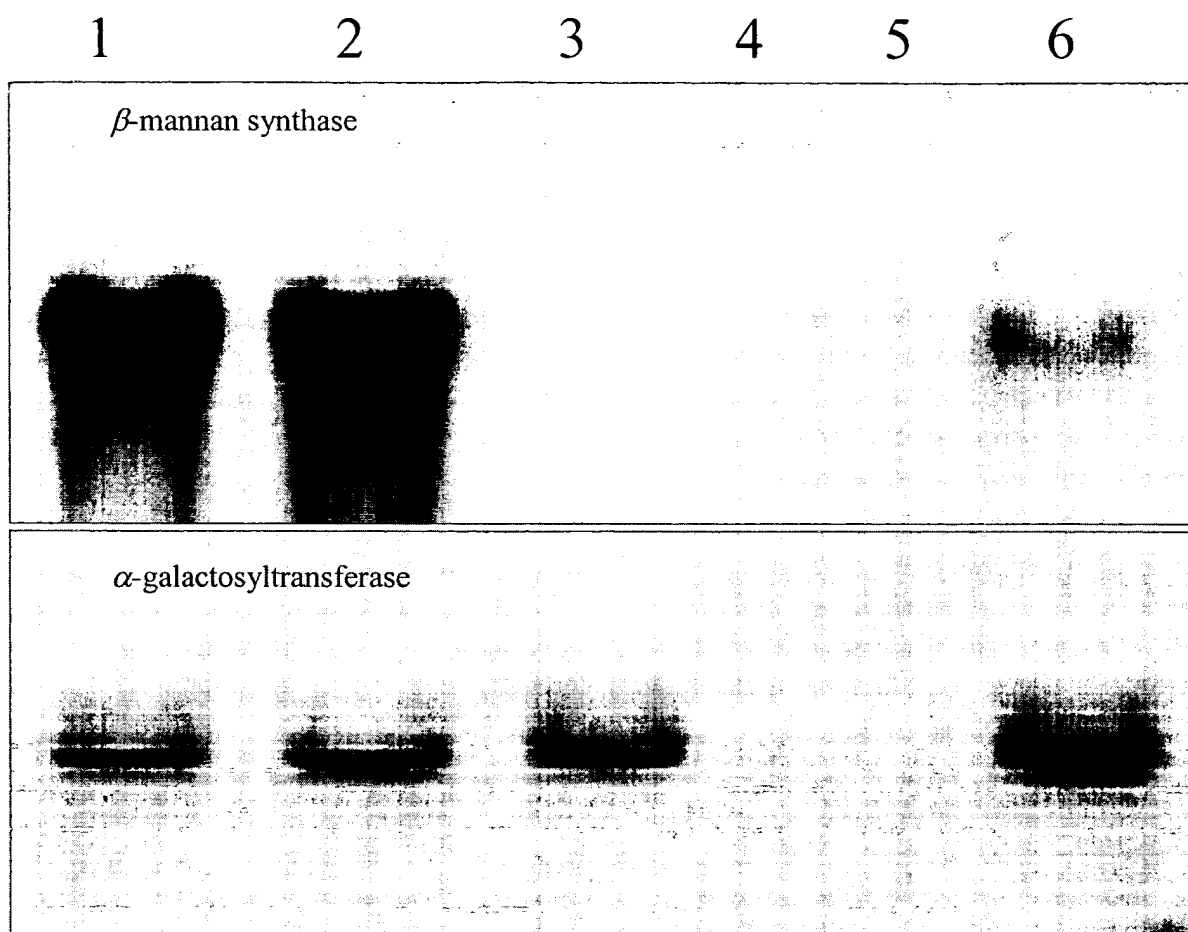


FIGURE 16

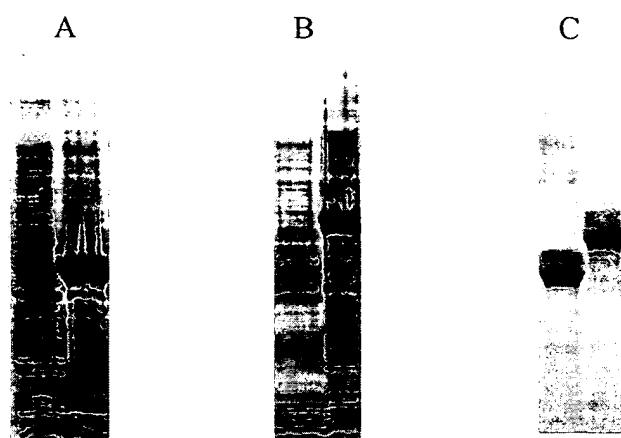


FIGURE 17

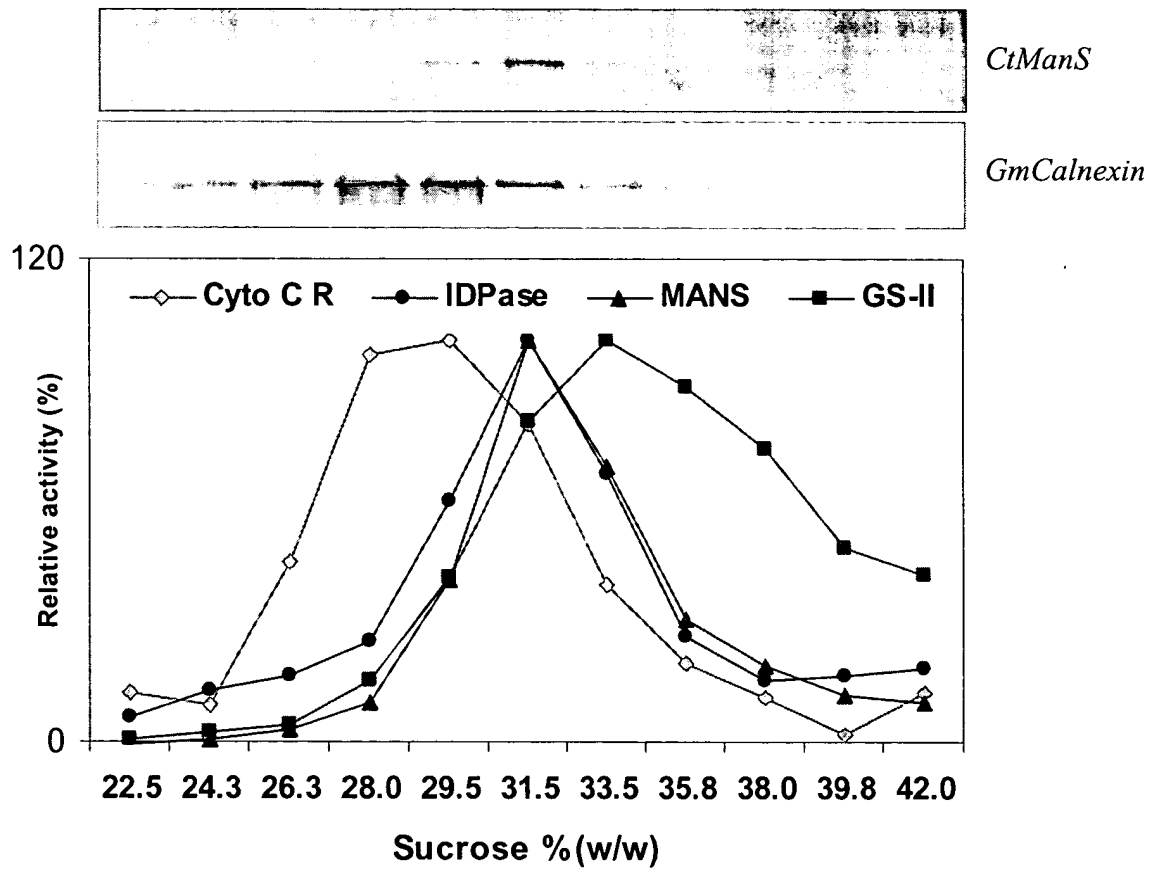


FIGURE 18

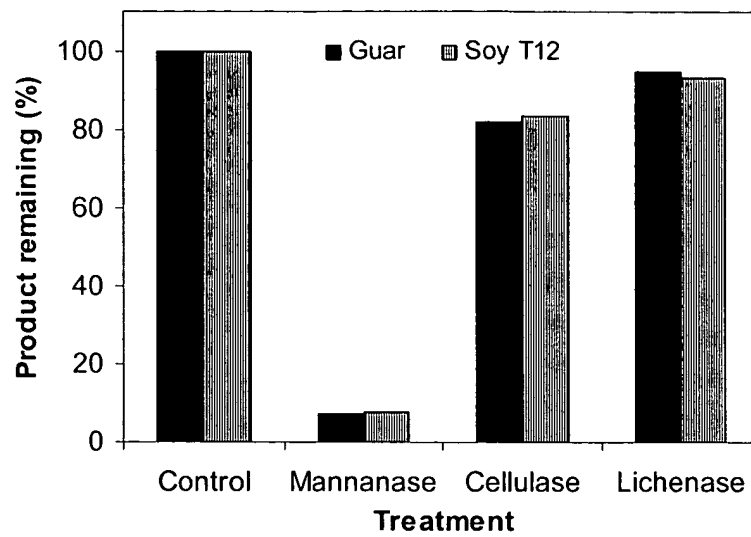


FIGURE 19

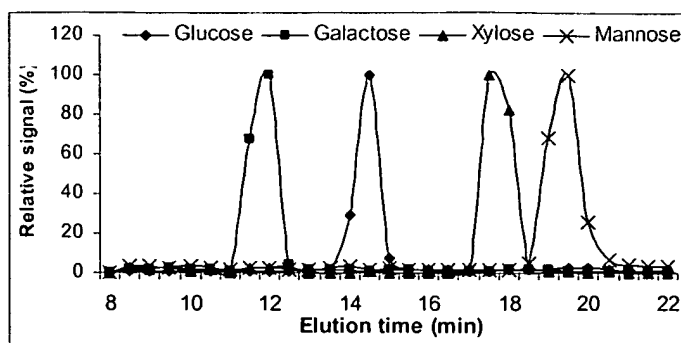


FIGURE 20A

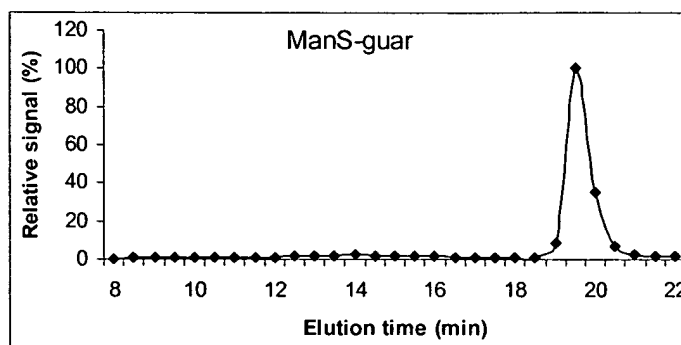


FIGURE 20B

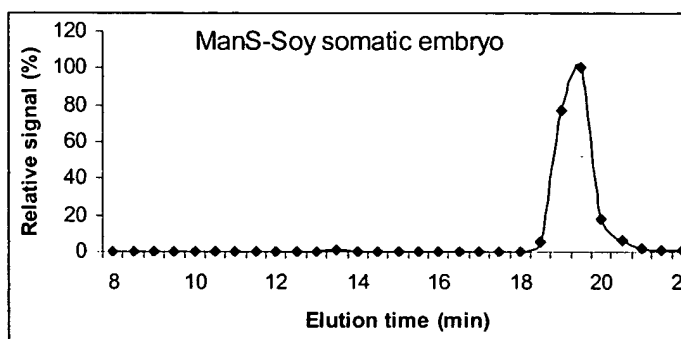


FIGURE 20C

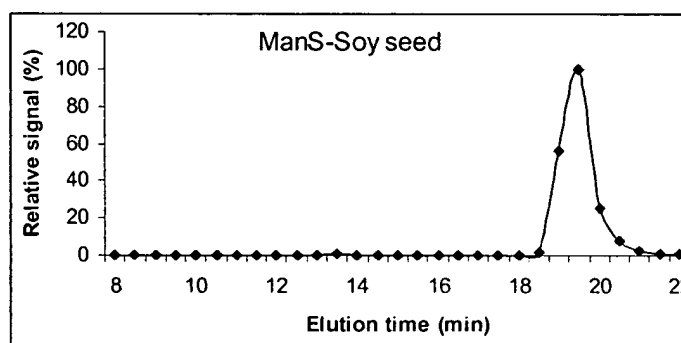


FIGURE 20D

FIGURE 20

>CiGonsT 1349 bp.

GGTGATGCAAATCGCATGAGAGGGGAAGAAGAGGTGTCTCACTTACTCTTCAATCTTCAT
TCACCCCTTACGAGTGCCACCTCTCTTCTCTCCTTCTCTTACAGCTCAAACAATTTGCTG
TTAAACCTTTGATCGGTTCATCCATGGAAGAAACCTTCGTTTTCCAGTGGAGCGTTATCAG
ATCTCTCTTGTCCATCCTTCAGTGGTGGGCTTTCAATGTCACCGTTATCATCGTTAACAA
GTGGATCTTCCAGAAATTGGATTTCAAGTTTCCCCTTTCAGTATCCTGTGTACACTTTAT
CTGCTCAGCAATTGGAGCATATATCGTGATTAAGGTGCTGAAGCTTAAACCACTGATAAC
TGTTGACCCGTATGATCGCTGGAGAAGAATATTTCTATGTCATTTGTATTCTGTATTAA
CATAGTGCTGGGGAATGTGAGCCTACGGTATATTCCAGTTTCTTTTATGCAGACGATAAA
GTCATTACGCCTGCAACTACAGTTGTTCTGCAATGGCTTGTATGGAGAAAGTATTTTGA
CTGGCGTATTTGGGCTTCTCTTATTCCCATTTGTTGGAGGGATTCTTCTTACATCTGTAAC
AGAGCTTAGTTTTAATATGTTTGGATTTTGTGCTGCCTTATTTGGTTGTTTGGCCACATC
TACGAAGACTATCCTTGCAGAATCTCTTTTGCATGGATACAAATTTGATAGCATAAACAC
AGTTTACTACATGGCACCCCTTTGCAACCATGATCTTGGCGCTTCCTGCCATGTTACTCGA
AGGAAATGGAATTCCTTGACTGGCTAAACACTCATCCATATCCTTGGTCAGCCCTCATCAT
TATTTTCAGCTCTGGGGTTTTGGCTTTCTGTCTCAACTTCTCCATTTTTTACGTGATTCA
CTCCACCACTGCTGTAACCTTTAACGTTGCCGGAACCTTAAGGTTGCAGTTGCTGTTCT
GGTTTCATGGCTGATATTTAGGAACCCAATATCATACTTAAATGCAGTTGGATGTGCCGT
GACACTTGTGGGATGTACATTCTATGGTTATGTAAGGCACATGCTCTCCCAACAGCCACC
AGTTCCAGGAACCTCTCGAACTCCAAGGACCCCTCGCAGTAAGATGGAGTTACTCCCTCT
TGTAATGATAAATTAGAAGATAAGGTCTAATTGTTTTAGCTATGTACACGAGGTTTATG
TCATTTCTAAGGCAGTAGTAACAGCAATATAGGTACAAAAGGATTACAGTGACTGGTTAT
TTATTCCGTTAGATTATCCCAAAATTTTCAATACAAGTTCTTTTACATTCCCTTTTTTAA
AAAAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 21

>CiGONST 0aa, 342 aa.

MEETFVFQWSVIRSLLSILQWWAFNVTVIIVNKWIFQKLDFKFPLSVSCVHFICSAIGAY
IVIKVLKLKPLITVDPDDRWRRIFFPMSFVFCINIVLGNVSLRYIPVSFMQTIKSFTPATT
VVLQWLVRKYFDWRIWASLIPIVGGILLTSVTELSFNMFGFCAALFGCLATSTKTILAE
SLLHGYKFDSINTVYYMAPFATMILALPAMLLEGNGILDWLNTHPYPWSALIIIFSSGVL
AFCLNFSIFYVIHSTTAVTFNVAGNLKVAVAVLVSWLIFRNPISYLNAGCAVTLVGCTF
YGYVRHMLSQQPPVPGTPRTPRTPRSKMELLPLVNDKLEDKV

FIGURE 22

	1		50
CtGONST	(1)	-----MEETTFVFWQSVIR-----	
AtGONST5	(1)	-----MEEGSLWRQWTMFR-----	
AtGONST4	(1)	-----MSSSRFDS-----	
AtGONST3	(1)	-----MSTNDEENGTVIEVKN--VPEP--SPE	
AtGONST2	(1)	MSAVKLEAIVCHEPDESELSHLSNDNGSKTKNGVVFQLLDQKSSEHRWFSE	
AtGONST1	(1)	-----MKLYEHDGVDLEDGKTVKSGG---DKP---IPR	
Consensus	(1)	MEGS ENGTVIR	
	51		100
CtGONST	(14)	-----SLLSILQWAFNVTVIIVNKKWIF	
AtGONST5	(15)	-----SLLSILQWGFNVTVIIMNKKWIF	
AtGONST4	(9)	-----NKQLTSSLVIGYALCSSLAVINKLAT	
AtGONST3	(24)	TWYS-----VFLRQASVYGVAAGYCLSAASLSIINKWAT	
AtGONST2	(51)	RFLRWRRRYLPVDGDNRRDHGSVKQSGPLVSGAAYCISSCSMIILNKIVL	
AtGONST1	(28)	KIH-----NR-----ALLSGLAYCISSCSMILVNKFVL	
Consensus	(51)	KQ SLLSILAYCISS SLIIINKWII	
	101		150
CtGONST	(37)	QKLDFKFPLSVSCVHFICSAIGAYIVIKVLKIKPLITVDPDDRWRRIFFPM	
AtGONST5	(38)	QKLDFKFPLSVSCVHFICSSIGAYIVIKVLKIKPLIVVDPEDRWRRIFPM	
AtGONST4	(37)	TYFNYPG--LLTALOYLCTVAVYLLGKSGLIN--HDPFTWDTAKKFLPA	
AtGONST3	(58)	MKEPYPG--ALTAMOYFTSAAGVLLCAQMKLIE--HDSLNLTLTWRFPLPA	
AtGONST2	(101)	SSYNFNAGVSLMLYQNLISCLVVAVLDISGVVS--VEKFNWKLIRVWMPV	
AtGONST1	(56)	SSYNFNAGIFLMLYQNFVSVIIVVGLSLMGLIT--TEPLTLRLMKVWFV	
Consensus	(101)	SKFNF A LSLS VQFI SAIGVYIL KMGLI ID D MRRFFPM	
	151		200
CtGONST	(87)	SFVFCINIVLGNVSLRYIPVSFMQTIKSFTPATTVVLQWLVWRK-VFDWR	
AtGONST5	(88)	SFVFCINIVLGNISLRYIPVSFMQTIKSFTPATTVVLQWLVWRK-VFDWR	
AtGONST4	(83)	AIVEYLAIFTNTNLLRHANMDTFIVFRSLTPLLVAIADTVFRSQPLPSRL	
AtGONST3	(104)	AMIFYLSLFTNSELLRHANMDTFIVFRSAVPIFVAIGETLFLHQPWPSVK	
AtGONST2	(149)	NVIFVGMLIVSGMYSLKYINVAMVTILKNATNLLTGIGEVYMERK-RQNNK	
AtGONST1	(104)	NVIFVGMLITSMFSLKYINVAMVTILKNVTNVTAVGEMYLENK-QHDNR	
Consensus	(151)	AVIF I IVTG SLRYINVA M VIKSLTPILTAIGE LVFRK Y D R	
	201		250
CtGONST	(136)	IWASLPIVGGILLTSVTELSFNMFGECAALFG-----CLATSTKTIL	
AtGONST5	(137)	IWASLVPIVGGILLTSITELSFNVFGCAALFG-----CLATSTKTIL	
AtGONST4	(133)	TELSLVVILAGAVGYVADSSFTLTAYSWALA-----YLVTTITEMVY	
AtGONST3	(154)	TWGLSLATIFGGSLLYVFLDYQFTIAAYSWALA-----YLVSMITDFVY	
AtGONST2	(198)	VWAAMFMMIISATSGGITDLTFDAVGYTWOLANCFLTASYSLTLRRVMDK	
AtGONST1	(153)	VWAALFLMIISAVSGGITDLSENNAVGYAWQTANCFLTASYSLTLRKTMDDT	
Consensus	(201)	IWASLVLIIGGALL ITDLSFNI GYSWALA Y LTLST MI	
	251		300
CtGONST	(179)	AESLLHGYKFDSENTVYYMAPFATMILALPAMLLEGNGILDWLNTHYPY-	
AtGONST5	(180)	AESLLHGYKFDSENTVYYMAPFATMILGLPAFLLERNGILDWFEAHPS-	
AtGONST4	(176)	IKHVMVSNIKLNIWGLVLYNNLLSLMIAPVFWFLTGEFTEVFAALSENNGN	
AtGONST3	(197)	IKHVMTIGLNTWGLVLYNNLEALLFPLELLIMGELKKIKHEITDET-D	
AtGONST2	(248)	AKQSTKSGSLNEVSMVLLNNLLSIPFGITLIILLGEWRYMISTDVTKD--	
AtGONST1	(203)	AKQVTOSGNLNEFSMVLLNNTLSLPLGLLSYFFNEMDYLYQTPLRL--	
Consensus	(251)	AK LL S KLNSW LVLYNNLLALMIG L ALLGE L T	

FIGURE 23a (1 of 2)

		301		350
CtGONST	(228)	---	WSALIIIFSSGVLAFCLNFSIFVVIHSTTAVTFNVAGNLKVAVAVLV	
AtGONST5	(229)	---	WSALIIILFNSGVLAFCLNFSIFVVIQSTTAVTFNVAGNLKVAVAVFV	
AtGONST4	(226)		LFEPYAFSSVAASCVFGLISYFGFAARNASATAFTVTGVNKFLLTVVI	
AtGONST3	(246)		WYSLOVLPVGLSCLFGLAISFFGFSCRRASATGFTVLGIVNKLLTVVI	
AtGONST2	(296)	---	SMFWVVATASGFLGLAISFTSMWFLHQTGPTTYSLVGSLNKVPISLA	
AtGONST1	(251)	---	PSFWMVMTLSGLLGLAISFTSMWFLHQTGATTYSLVGSLNKIPLSLA	
Consensus	(301)		SAWIIIV ASGVLGLAISFS FW IHATSATTFSVVG LNKIL VLI	
		351		400
CtGONST	(275)	SW	IFRNPISYINAVGCAVTLVGCTFYGYVRHMLSQQPPVPGTPRTPRTP	
AtGONST5	(276)	SW	MIFRNPISPMNAVCGITLVGCTFYGYVRHMLSQQQ--PGTPRTPRTP	
AtGONST4	(276)	NV	TIWDKHATPVGLVCLFTTCGGVGYQQSVKLDKPIEKVSEKDSEKGEE	
AtGONST3	(296)	NM	WWDKHSTFVGTTEGLVCMFGGVMYQOSTEK-KPNATQEAQPKQEQDEE	
AtGONST2	(343)	GL	VLFNVPISLPNLFSTLFLGLFAGVVFARAKMS-----	
AtGONST1	(298)	GL	VLFNVPISLQNSASTLFLGLVAGVVFARAKMREKS-----	
Consensus	(351)	LLIF	PIS VNAVGLFTLVGGVVYA AKMM K Q G P	
		401		430
CtGONST	(325)	RSKMEL	PLVNDKLEDKV-----	
AtGONST5	(324)	RNKMEL	PLVNDKLESKE-----	
AtGONST4	(326)	DE--	ELTQLVPGKLASVV-----	
AtGONST3	(345)	QE--	KLTEMQENKESNSVDIKETLKSEEKL	
AtGONST2	(376)		-----	
AtGONST1	(334)		-----	
Consensus	(401)	ELL	LV KL V	

FIGURE 23b (2 of 2)

	CtGONST	AtGONST5	AtGONST4	AtGONST3	AtGONST2	AtGONST1
CtGONST	100	90	31	24	16	28
AtGONST5		100	31	22	17	28
AtGONST4			100	51	19	28
AtGONST3				100	17	26
AtGONST2					100	59
AtGONST1						100

FIGURE 24

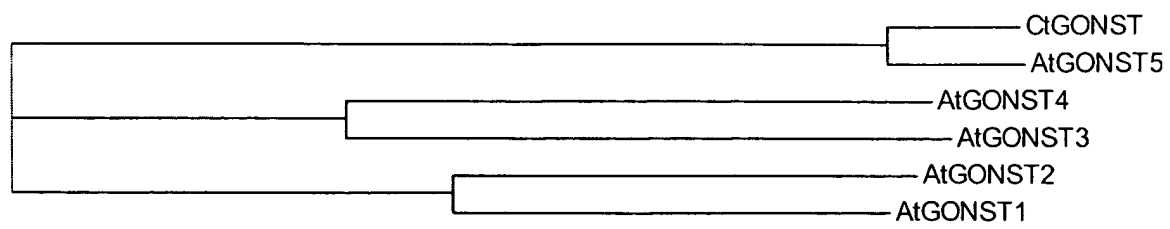


FIGURE 25

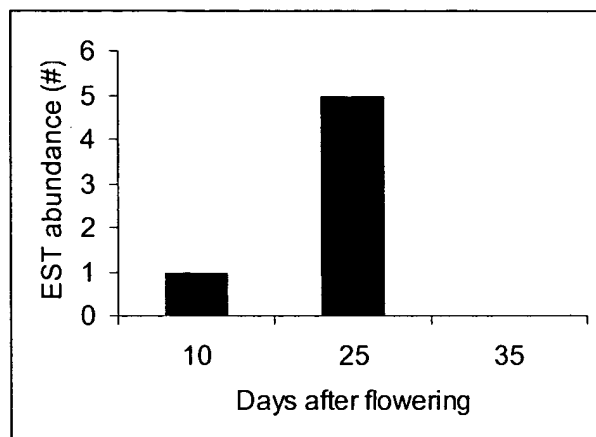
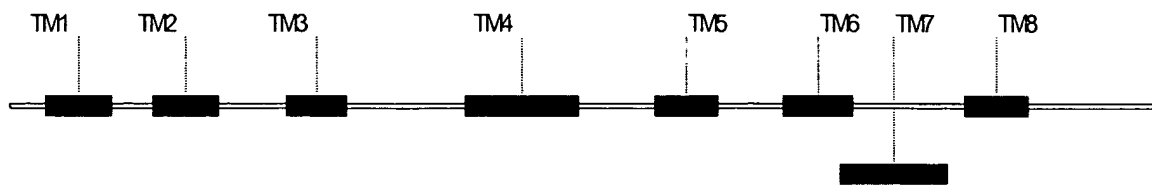


FIGURE 26



CtGONST
342 aa

FIGURE 27